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Cond

6. (Amended) Process according to claim 2, characterized in that site correlation values within each of the sequences within the first group and/or site correlation values within each of the sequences within the second group(s) are determined and said site correlation values are used for the calculation of the probability of interaction and/or for the calculation of the predicted interaction value of the sequence represented bimolecules.

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8. (Amended) Process according to claim 2, characterized in that each sequence of each of said groups is fused to each other to form fused sequences comprising at least one sequence of the first group and at least one sequence of any second group(s),

the correlation values within these fused sequences are determined, and the correlation values are used as group correlation values for determining the predicted interaction value and/or the probability of interaction.

9. (Amended) Process according to claim 2, characterized in that correlation values are determined by creating a position specific matrix containing the distances between pairs of sequences at that position whereby the distances are calculated by applying a standard distances matrix, creating a combined matrix for two positions by calculating the covariation coefficient between equivalent positions of their position specific matrices, and determining the correlation value for a pair of positions by averaging the correlation values of the combined matrix.

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13. (Amended) Method according to claim 11, characterized in that the elements the predicted interaction value of which is positive, are interacting bimolecules.

14. (Amended) Method according to claim 11, characterized in that any of second set(s) of data is converted into the first set of data and the first set of data is converted into a second set of data, and group correlation values are determined between the sequences of this new first set of data and the sequences of any of the second set(s).

15. (Amended) Method according to claim 11, characterized in that site correlation values within each of the sequences within the first set of data and/or site correlation values within each of the sequences within the second set(s) of data are determined, and said site correlation values form a set-specific site correlation value data set.

17. (Amended) Method according to claim 15, characterized in that the site correlation values are correlation values for substitutions within the sequences.

18. (Amended) Method according to claim 11, characterized in that a fused element set of data is generated by combining each element of the first set of data individually with each element of any of the second sets(s) of data, and attributing each fused element individually to the fused element set of data.

20. (Amended) Method according to claim 11, characterized in that the correlation values are determined by creating a position specific matrix containing the distances between pairs of sequences at that position whereby the distances are calculated by applying a standard distances matrix, creating a combined matrix for two position by calculating the covariation coefficient between equivalent positions of their positions specific matrices, and determining the correlation value for a pair of positions by averaging the correlation values of the combined matrix.

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22. (Amended) Method according to claim 11, characterized in that the first set of data and/or second the second set(s) of data are retrieved from a medium which is selected from the group comprising databanks, linked databanks, textual data and sets of data generated by an analytical instrument.

23. (Amended) Method according to claim 11, characterized in that the set(s) of data comprise aligned sequences.

24. (Amended) Method according to claim 11, characterized in that the output data are output control characters for a target medium.

25. (Amended) Method or process according to claim 2, characterized in that the sequences of the first group or second group(s) or first set of data or second set(s) of data are selected from the group comprising DNA sequences, RNA sequences and amino acid sequences.

26. (Amended) Method or process according to claim 2, characterized in that the number of sequences comprised in any of the groups or any of the sets of data is at least, preferably at least 11.

27. (Amended) Method or process according to claim 2, characterized in that the sequences are homologous sequences.

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30. (Amended) Method or process according to claim 27, characterized in that the homologous sequences are homologous genes.

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32. (Amended) Use of the method according to claim 11 for the simulation of biomolecule interaction.

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34. (Amended) Pairs of interacting bimolecules determined according to a method or process according to claim 2.

35. (Amended) Data structure readable by a computer, said data structure being generated by a process or a method according to claim 2.

36. (Amended) Computer readable medium for embodying or storing therein data readable by a computer, said medium comprising one or more of the following: a data structure generated by executing a process or a method according to claim 2; Computer program code means which is adapted to cause a computer to execute a process or method according to claim 2.

38. (Amended) Database containing information on interacting sequence pairs generated by applying the process or method according to claim 2.

40. (Amended) Computer system comprising an execution environment for running the process or method according to claim 2.

41. (Amended) Device for simulating the interaction of bimolecules represented by their sequences which comprises a loading device for making available the sets of data according to claim 11, a processing device for performing the method according to claim 11, an output device for receiving the output data generated by the processing device.